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FIG. 1 - 1

Set I.

V <sub>H</sub> 4-39						D6-13						J <sub>H</sub> 5											
C	A	R	H/Q	TGT	GGG	AGA	CA	C	A	S	R	G	Y	S	S	W	Y	S	S	N	W	F	D
TGT	GGG	AGC	TCC	AGA	GGG	TAT	AGC	GGC	TAT	AGC	GGC	TGG	TGG	TAC	W	W	-	S	S	N	W	F	D
C	A	R	H	L	G	Y	S	S	S	S	S	W	Y	TAT	GGG	GCA	GCC	AAC	TGG	TTC	GAC	CLL039	
TGT	GGG	AGA	CAT	CTG	CGA	TAT	AGC	GGC	TAT	AGC	GGC	TGG	TAT	Y	G	A	A	N	W	F	P	D	
C	A	R	R	F	G	Y	S	S	S	S	S	W	Y	-	G	L	D	W	P	F	P	D	
TGT	GGG	AGA	CGG	TTC	GGG	TAT	AGC	GGC	TGG	TAT	AGC	GGC	TGG	TAC	W	Y	S	W	R	N	W	F	D
C	A	R	S	T	G	A	S	S	S	S	S	W	Y	TAT	TCT	TGG	CGC	AAT	TGG	TTC	GAC	CLL114	
TGT	GGG	AGG	TCG	ACC	GGG	TAT	AGC	GGC	TAT	AGC	GGC	TGG	TAC	TAC	W	Y	S	W	R	N	W	F	D
C	A	R	Q	A	G	Y	S	S	S	S	S	W	Y	G	P	S	N	W	F	P	S	D	
TGT	GGG	AGA	CAA	GCT	GGG	TAT	AGC	GGC	TAT	AGC	GGC	TGG	TAC	TAC	GGC	CCC	TCC	AAC	TGG	TTC	GAC	CLL209	
C	A	R	H	E	G	Y	S	S	S	S	S	W	Y	-	R	S	D	W	F	P	D		
TGT	GGG	AGA	CAT	GAG	GGG	TAT	AGC	GGC	TAT	AGC	GGC	TGG	TAC	---	AGG	AGC	GAC	TGG	TTC	GAC	Y092449	immunocytoma	

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FIG. 1 - 2

Set II.

V <sub>H</sub> 4-34										J <sub>H</sub> 6									
C A R G					V D T					D5-5					AT TAC TAC TAC				
TGT GCG AGA GG					GAT GAT GAT GAT					GCT GAT ACA GAT					GTC ATG GTT AC				
C A R G	V D T	P T I	R Y Y	Y Y Y	C C T A C T A C T	A C T A C T A C T	G C G T A C T A C T	T A C T A C T A C T	A T A C T A C T A C T	C L L 1 8 3	C L L 2 4 0	C L L 3 4 2	A F 0 8 7 4 2 2	C L L 4 B	1	A U 2 3 9 3 3	I D 4 7	2	
TGT GCG AGA GG	GAT GAT GAT GAT	GCT GAT ACA GAT	GTC ATG GTT AC	C C T A C T A C T	A C T A C T A C T	G C G T A C T A C T	T A C T A C T A C T	A T A C T A C T A C T	C L L 1 8 3	C L L 2 4 0	C L L 3 4 2	A F 0 8 7 4 2 2	C L L 4 B	1	A U 2 3 9 3 3	I D 4 7	2		
TGT GCG AGA GG	GAT GAT GAT GAT	GCT GAT ACA GAT	GTC ATG GTT AC	C C T A C T A C T	A C T A C T A C T	G C G T A C T A C T	T A C T A C T A C T	A T A C T A C T A C T	C L L 1 8 3	C L L 2 4 0	C L L 3 4 2	A F 0 8 7 4 2 2	C L L 4 B	1	A U 2 3 9 3 3	I D 4 7	2		
TGT GCG AGA GG	GAT GAT GAT GAT	GCT GAT ACA GAT	GTC ATG GTT AC	C C T A C T A C T	A C T A C T A C T	G C G T A C T A C T	T A C T A C T A C T	A T A C T A C T A C T	C L L 1 8 3	C L L 2 4 0	C L L 3 4 2	A F 0 8 7 4 2 2	C L L 4 B	1	A U 2 3 9 3 3	I D 4 7	2		
TGT GCG AGA GG	GAT GAT GAT GAT	GCT GAT ACA GAT	GTC ATG GTT AC	C C T A C T A C T	A C T A C T A C T	G C G T A C T A C T	T A C T A C T A C T	A T A C T A C T A C T	C L L 1 8 3	C L L 2 4 0	C L L 3 4 2	A F 0 8 7 4 2 2	C L L 4 B	1	A U 2 3 9 3 3	I D 4 7	2		

## FIG. 1 - 3

Set VIa.

	V <sub>H1</sub> -02	D6-19	J <sub>H4</sub>
C	A	R	D/E
TGT	GGC	AGA	GA
	V	Q	W
	GG	GTA	TAG
	GG	CAG	TGG
	GG	GTA	GTC
C	A	R	E
TGT	GGC	AGG	GAG
	A	R	V
	V	Q	W
	GG	GTC	TGG
	GG	GTC	TGG
C	A	R	E
TGT	GGC	AGA	GAG
	A	R	E
	V	Q	W
	GG	GCA	CAG
	GG	GCA	CAG
C	A	R	E
TGT	GGC	AGG	GAG
	A	R	V
	V	Q	W
	GG	GAG	CAG
	GG	GAG	CAG
C	A	R	E
TGT	GGC	AGG	GAG
	A	R	V
	V	Q	W
	GG	GAG	CAG
	GG	GAG	CAG
C	A	R	N
TGT	GGC	AGA	AAC
	A	R	E
	E	Q	W
	GG	CAG	TGG
	GG	CAG	TGG
C	A	R	E
TGT	GGC	AGA	GAG
	A	R	E
	E	Q	W
	GG	CAG	TGG
	GG	CAG	TGG

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## FIG. 1 - 4

Set VIB,c,d

VH1-03	D6-19	JH4	Y	F	D	Y
C A R D/E						
TGT GCG AGA GA						
V V V	Q Q Q	W W W	L L L	V V V		
GG GTA TAG CAG	TGG CTG GTC	TGG CTG GTC	CTA TCT	TAC TTT GAC	TAC TAC	
C A R E	Q Q Q	W W W	L L L	S S S	- - -	
TGT GCG AGG GAG CAG	TGG CTG GTC	TGG CTG GTC	CTA TCT	TAC TTT GAC	TAC TAC	CLL336
C A R E	Q Q Q	W W W	L L L	V V V	N N N	
TGT GCG AGG GAG CAG	TGG CTG GTC	TGG CTG GTC	CTA TCT	AAC TAC TTT GAC	TAC TAC	CLL360
C A R E	Q Q Q	W W W	L L L	A A A	L L L	
TGT GCG AGA GAG CAG	TGG CTG GTC	TGG CTG GTC	GCC TTA AAA	CCC TTT GAC	TAC TAC	AF376961 LAN Digheiro
C A R K Q	W W W	L L L	A A A	I I I	V V V	
TGT GCG AGA AAG CAG TGG CAG TGG CTC	GCC ATC GTC AAC TAC TAC	TGG CTC	CTA TCT	TAC TTT GAC	TAC TAC	L01278 CLL-412 3
C A R E Q	W W W	L L L	G G G	P P P	- - -	
TGT GCG AGA GAG CAG TGG CTC	GCG CTC	GCG CTC	CTA CCT	ACC TTT GAC	TAC TAC	U86801 4 U3/1
C A R V Q	W W W	L L L	G G G	T T T	G G G	
TGT GCT AGG GTT CAG TGG CTC	GCG CTC	GCG CTC	AGC GGG	CGG AAT GAC	TAC TAC	U84176 KEM (VH1-46) 5 U0
C A R G Q	W W W	L L L	V V V	I I I	L L L	
TGT GCG AGG GGA CAG TGG CTC	GCG CTC	GCG CTC	ATC CTA	ACC TTT GAC	TAC TAC	U84162 BYR (VH1-46) 5 U0
C A R D Q	W W W	L L L	P P P	T T T	N N N	
TGT GCG AGA GAT CAG TGG CTC	GCG CTC	GCG CTC	ACG ACG	AAA AAC TTT GAC	TAC TAC	AF376953 Digheiro PIQ U2
C A R E Q	W W W	L L L	V V V	L S S	- - -	
TGT GCG AGG GAG CAG TGG TGG	TGG GTC	TGG GTC	CTA TCT	CAC TTT GAC	TAC TAC	CLL154 (VH1-18)

**FIG. 1 - 5**

Set IV.

V <sub>B</sub> 1-69				D3-16				J <sub>B</sub> 3			
C	A	R	D/E	C	A	R	D	D	A	F	D
TGT	GGG	AGA	GA	Y	Y	D	Y	Y	W	G	Y
				G	TAT	TAT	GAT	TAC	GTT	TGG	GGG
C	A	R	G	G	G	D	Y	V	W	G	S
TGT	GGG	AGA	GA	GGG	GAT	TAT	GAT	TAC	GTT	TGG	GGG
C	A	R	G	G	I	Y	D	Y	V	W	G
TGT	GGG	AGA	GGG	GGG	GGT	ATT	TAT	GAT	TAC	GTT	TGG
C	A	R	G	G	G	N	Y	D	Y	I	W
TGT	GGG	AGA	GA	GGG	GGC	AAT	TAT	GAT	TAC	ATT	TGG
C	A	R	G	G	D	Y	D	Y	V	W	G
TGT	GGG	AGA	GGG	GGG	GAT	TAT	GAT	TAC	GTT	TGG	GGG
C	A	R	G	G	N	Y	D	Y	D	I	W
TGT	GGG	AGA	GA	GGG	AAT	TAT	GAT	TAC	ATT	TGG	GGG
C	A	R	G	G	D	Y	D	Y	V	W	G
TGT	GGG	AGA	GGG	GGG	GAT	TAT	GAT	TAC	GTT	TGG	GGG
C	A	R	G	G	N	Y	D	Y	D	I	W
TGT	GGG	AGA	GA	GGG	AAT	TAT	GAT	TAC	ATT	TGG	GGG

*J*-cardiolipin  
Martin, France

*α*-cardiolipin

Martin, France

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## FIG. 1 - 6

Set V.

V <sub>H1-69</sub>			D3-10			J <sub>H5</sub>		
C	A	R	D/E				Y	Y
TGT	GCG	AGA	GA				AT	TAC
	I	T	M	V	R	G	T	TAC
GT	ATT	ACT	ATG	GTT	CGG	GGA	ATT	ATA
							AC	
C	A	E	G	M	V	Q	G	I
TGT	GCG	GAG	GGT	ATG	GTT	CAG	GCA	ATT
C	A	R	S	M	V	Q	G	V
TGT	GCG	AGG	TCT	ATG	GTT	CAG	GGA	ATT
C	A	R	A	M	V	R	G	I
TGT	GCG	AGG	GCT	ATG	GTT	CGG	GGA	ATT
C	A	R	V	M	V	R	G	V
TGT	GCG	AGA	GTT	ATG	GTT	CGG	GGA	GTT

SIN Digheliro U0 AF376959 AF376959 SIN Digheliro U0

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FIG. 1 - 7

Set III.

V <sub>H</sub> 3-21		J <sub>H</sub> 6	
C	A	R	E/D
TGT	GCG	AGA	GA
Y	Y	Y	Y
AT	TAC	TAC	TAC
C	A	R	D
TGT	GCG	AGA	GAT
C	A	R	D
TGT	GCG	AGA	GAT
C	A	R	D
TGT	GCG	AGA	GAT
C	A	S	D
TGT	GCG	AGC	GAT
C	A	R	E
TGT	GCG	AGA	GAG
C	A	R	D
TGT	GCG	AGA	GAT
C	A	R	D
TGT	GCG	AGA	GAT
C	A	R	D
TGT	GCG	AGA	GAT

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FIG. 1 - 8

FIG. 1 - 9

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FIG. 2

*Amino acid alignments of the H chain variable regions of all sequences in each Set*

Set	CDR1	CDR2	CDR3
Set IV			
Germline	QVQLVQSGAEVKPGSSVKVSCKASGGTPSSYIAISWVRQAPGQGLEMWGIIPIFGTANIAQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARD	YDYYWGGSYRY DAEDVWGGTMTVSS	
CLL068	.....	.....	GGD.....SN.....
CLL258	.....	.....	GGI.....PN.....
MP9	.....	.....	GGP.....PN.....
SM1	.....	.....	GGW...I...SN.....
CLL022	.....	.....	GGD.....PN.....I
RI8	.....	.....	GGR...I...SN.....V
Consensus	QVQLVQSGAEVKPGSSVKVSCKASGGTPSSYIAISWVRQAPGQGLEMWGIIPIFGTANIAQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARGGDDYDVNGGSYRNADPFDINGGGTAVTVSS		
Set VIII	CDR1	CDR2	CDR3
Germline	QVQLVQSGAEVKPGSSVKVSCKASGGTPSSYIAISWVRQAPGQGLEMWGIIPIFGTANIAQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARD	DIVVVPAAI YYYYYGMDVWGGTIVTVSS	
PS41	.....	.....	GG.....MS.....
UCR4	.....	.....	GA.....HG.....
GO13	.....	.....	GG.....MR.....
Consensus	QVQLVQSGAEVKPGSSVKVSCKASGGTPSSYIAISWVRQAPGQGLEMWGIIPIFGTANIAQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARGGDDYDVNGGSYRNADPFDINGGGTAVTVSS		
Set V	CDR1	CDR2	CDR3
Germline	QVQLVQSGAEVKPGSSVKVSCKASGGTPSSYIAISWVRQAPGQGLEMWGIIPIFGTANIAQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARD	YYYYYGMDVWGGTIVTVSS	
CLL561	.....	.....	AM.Q...Y...V...K...
MJ21	.....	.....	A.....Y...X...E...
RF22	.....	.....	G.....Y...X...E...
GN12	.....	.....	EG...Q...G...
FUH	.....	.....	S.Q...NVL...
ID64	.....	.....	A...HLD...Y...X...
SIN	.....	.....	V...SLD...Y...X...D...
Consensus	QVQLVQSGAEVKPGSSVKVSCKASGGTPSSYIAISWVRQAPGQGLEMWGIIPIFGTANIAQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARGGDDYDVNGGSYRNADPFDINGGGTAVTVSS		
Set XII	CDR1	CDR2	CDR3
Germline	QVQLQWAGGLLKEPSETLSLTCAVYGGTSGYIYMWIROPPGKGLEWIGEINHGSTNTYPSLKEVTLISVDTSKNQPSLKLSSVTAADTAVYTCARD	YDYYWGMDVGGTIVTVSS	
CLL183	...L.....	...T...S.....	...N.....IG...ENLR...
CLL240	.....	...E.....	...A.I...Y...V...R...
CLL342	.....	...E.....	...T...E...NG...PLR...
CLL48	...A...P.....	...HS...R.....	...K...A.Y...P...RR...
ID67	...VD.....	...DAS...N...L.....	...I...P...DVIKR...P...
Consensus	QVQLQWAGGLLKEPSETLSLTCAVYGGTSGYIYMWIROPPGKGLEWIGEINHGSTNTYPSLKEVTLISVDTSKNQPSLKLSSVTAADTAVYTCARGGDDYDVNGGSYRNADPFDINGGGTAVTVSS		
Set VIIa	CDR1	CDR2	CDR3
Germline	QVQLVQSGAEVKPGASVKVSCKASGYTTGTYIYMWIRQAPGQGLEMWGWINPNSGGTNTYQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARD	YDYYWGQGTIVTVSS	
CLL011	.....	.....	H...LKH...
CLL266	.....	.....	E...GAEN...
CLL270	.....	.....	V...GLRH...
CLL340	.....	.....	S...LKN...
CLL3	.....	.....	V...LLEH...
SLv18	.....	.....	N...GLD...
CLL-H2B	.....	.....	E...RTG...
Consensus	QVQLVQSGAEVKPGASVKVSCKASGYTTGTYIYMWIRQAPGQGLEMWGWINPNSGGTNTYQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCAREQWLVLEN-YDYYWGQGTIVTVSS		
Set VIIb	CDR1	CDR2	CDR3
Germline	QVQLVQSGAEVKPGASVKVSCKASGYTTGTYIYMWIRQAPGQGLEMWGWINPNSGGTNTYQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARD	YDYYWGQGTIVTVSS	
CLL336	.....	.....	E...LS...
CLL360	...N.....	...IT.....	E...L...
LAN	.....	.....	E...ALK-P...
CLL-412	.....	...T...V.....	K...AVN...
POR	.....	.....	S...GLP-T...
PTQ	.....	...G.....	PTM-N...
Consensus	QVQLVQSGAEVKPGASVKVSCKASGYTTGTYIYMWIRQAPGQGLEMWGWINPNSGGTNTYQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCAREQWLVLEN-YDYYWGQGTIVTVSS		
Set VIC	CDR1	CDR2	CDR3
Germline	QVQLVQSGAEVKPGASVKVSCKASGYTTGTYIYMWIRQAPGQGLEMWGWINPNSGGTNTYQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARD	YDYYWGQGTIVTVSS	
CLL154	.....	.....	E...LSH...
Set VId	CDR1	CDR2	CDR3
Germline	QVQLVQSGAEVKPGASVKVSCKASGYTTGTYIYMWIRQAPGQGLEMWGWINPNSGGTNTYQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARD	YDYYWGQGTIVTVSS	
BYR	.....	.....	IIN...
KEM	.....	.....	VGLTGPY...
Consensus	QVQLVQSGAEVKPGASVKVSCKASGYTTGTYIYMWIRQAPGQGLEMWGWINPNSGGTNTYQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCAREQWLVLEN-YDYYWGQGTIVTVSS		
Set VIe	CDR1	CDR2	CDR3
Germline	EVQLVQSGAEVKPGESLRISCKGGTFTSYIYMWIRQAPGQGLEMWGWINPNSGGTNTYQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCARD	YDYYWGQGTIVTVSS	
CLL026	.....	.....	GGD...
TRB	...Q...	.....	...
CLL021	.....	...E...	R...ALCH...
ID38	.....	...G...	...PGVY...
GO14	.....	...I...Y...G...P...R...	...LP...
AG	.....	.....	E...IVTH...
HOW	.....	.....	...LD...
Consensus	EVQLVQSGAEVKPGESLRISCKGGTFTSYIYMWIRQAPGQGLEMWGWINPNSGGTNTYQKFQGRVTTADKSTSTAYMELSSLRSEDATAVYTCAR		

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FIG. 3

*Amino acid alignments of the L chain variable regions of all sequences in each Set.*

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FIG. 4

V <sub>H</sub> -69	D3-16	J <sub>H</sub> 3	V <sub>K</sub> A27	J <sub>K</sub> 1/4*/5*
C A R D E		D A F D I	Q Q Y G S S P P	
tgt gct aga ga		tgt gct tct gat atc	dag cgt tat gct aca cct cc	
Y Y D Y V W G S Y R Y			W T F G	
g tat bat gnt tac gct tgg agg agt bat cgt bat acc			g tag acg tcc agg	
			CLL068	
G G D . . . . .		S N . . . . .		
ga agg g . . . . .		cc . B . . . . .		
G G I . . . . .		P N . . . . .	CLL258	
gg ggt at . . . . .		ccg . a . . . . .		G . . . . .
G G P . . . . .		P N . . . . .	MF9	
ga ggg cc . . . . .		ccg . a . . . . .		P . . . . .
G G N . . . . .		I . . . . .		
ga ggg a . . . . .		S N . . . . .	SMI	
G G D . . . . .		cc . a . . . . .		
gg ggt g . . . . .		P N . . . . .	CLL022 (natural Ab producing clone)	
G G N . . . . .		ccg . a . . . . .		
ga ggg a . . . . .		I . . . . .		$\alpha$ -cardiolipin
		S N . . . . .		
		cc . a . . . . .		

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FIG. 5

V <sub>H1</sub> -69	D2-2	J <sub>H6</sub>	V <sub>KL6</sub>	J <sub>K3</sub>
C A R D/E tgt gcg aga ga	D I V V V P A A T ag gat att gta gta cca gct gct ata cc	Y Y Y at tac tac tac	Q Q R S N W P P cag cag cgt aac tgg aac tgg cct cc	F T F G P G a ttg act ttc ggc cct sgg
• • • G G . . . . .	• • • G A . . . . .	• • • M S - - -	• • • M G - - -	FS41 UCA4
• • • G G . . . . .	• • • G G . . . . .	• • • M R - - -	• • • M R - - -	GO13 G . . . . .
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18				1 2 3 4 5 6 7 8 9 10

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FIG. 6

V <sub>3</sub> 1-69	D3-10	J <sub>4</sub> 6	V <sub>1</sub> -16	J <sub>1</sub> 1/3*
C A R D/E			W D D S L N G P	
tgt gcg aga ga			tgg gat gag aat ggt cc	
I T M V R G V I I			Y V F G	
gt att actg gtt cgg gga gtt att ataa ac			t tag gtg ttc ggc	
• • . A . . Q . . . Q T . . . CII561				
• . . . . a. . . . . a. . . . . a.				
• . . A . . . . . . T Y . . . MJ21				
• . . . . . . . . . . ct t. . . . .				
• . . G . . . . . . T Y . . . RF22				
• . . . . . . . . . . ct t. . . . .				
• . . E G . . . . . . G I . . . GEN12				
• . . . . . . . . . . gg. t. . . . .				
• . . S . . . . . . N V L . . . FUH				
• . . . . . . . . . . ac gtc ct. . . .				
• . . A . . . . . . H L D . . . ID64				
• . . . . . . . . . . ctc trg g. . . .				
• . . V . . . . . . S L D . . . SIN				
• . . . . . . . . . . tcc atgg g. . . .				

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FIG. 7

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FIG. 8

V <sub>H</sub> 1-02	D6-19	J <sub>H</sub> 4	V <sub>K</sub> 012/O2	J <sub>K</sub> 1/2*
C A R D/E		Y F D Y	Q Q S Y S T P P	
tgt gag aga ga		ac tac ttt gaa tac	caa cgg agt tac agt acc cct cc	
V * Q W L V				W T F G
gg gta tag cag tgg atg gta c			g tgg acc ttc ggc	
L E H . . . . .	CLL011	. . . . .	T . . . . .	
ttt gag . . . . .		g ac . . . . .		
G A E - N . . . .	CLL266	. . . . .	- K . . . . .	
gaa gaa . . . . .		g . . . . .		
V . . . G L R - H . . . .	CLL270	. . . . .		
gc tta cga . . . . .				
L K - N . . . . .	CLL340	. . . . .		
tg aac . . . . .				
V . . . L L E - R . . . .	CLL3			
tt . . . t.a . . . . .				
G L D . . . . .	sv18 (marginal zone lymphoma)			
a.c . . . . .				
E . . . R T - S . . . .	CLL-H2B			
agg acg . . . . .				
L S - . . . . .	CLL336	. . . . .	S . . . . .	
ta tot . . . . .		g . . . . .		
L - N . . . . .	CLL360	. . . . .		
tt . . . . .				
A L K - P . . . . .	LAN			
cc tta aaa . . . . .				
K . . . A I V N . . . . .	CLL-412	. . . . .		
aa . . . . .		g . . . . .		
P T - N N . . . . .	PIQ			
cc acg . . . . .				
L S - H . . . . .	CLL154	. . . . .		
ta tot . . . . .				
G . . . I L - N . . . . .	BYR			
aa . . . . .				
V . . . G L T G P N . . . .	KEM			
tg acg ggg cgg aa . . . .				
G G - D . . . . .	CLL026			
gt ggg . . . . .				
R . . . A L - G H . . . . .	TRE	. . . . .		
ag . . . . .				
F G V - Y . . . . .	CLL021			
aa . . . . .				
L P - . . . . .	ID38			
tt cca . . . . .				
E . . . I V T - H . . . . .	GO14	. . . . .	- R . . . . .	
aa . . . . .		agg . . . . .		
L - D . . . . .	AG			
ttg . . . . .				
E . . . L S - . . . . .	HOW			
nuclotide sequence not available				
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15		1 2 3 4 5 6 7 8 9 10 11 12 13		